AMENDMENTS TO THE CLAIMS:

Please amend the claims as follows:

1. (Original) An isolated nucleic acid molecule consisting of SEQ ID NO 1, its complementary form and the RNA form thereof.

2. (Original) An isolated nucleic acid molecule consisting of SEQ ID NO 2, its complementary form and the RNA form thereof.

3. (Previously Presented) An isolated nucleic acid molecule of more than 10 contiguous nucleotides that specifically hybridizes to SEQ ID NO 1 or 2, or to the RNA form of said SEQ ID NO 1 or 2 wherein T is replaced by U, or to the complementary form of said SEQ ID NO 1 or 2, or to a fragment of at least 20 contiguous nucleotides thereof, or to any of their homologues, for the detection and/or identification of *Enterococcus* species.

4. (Original) An isolated nucleic acid molecule according to claim 3 consisting of a nucleic acid selected from the group consisting of SEQ ID NO 22 to 26, 28 to 43, 45 to 65 and 67 to 84.

5. (Previously Presented) A set of two or three polynucleotide probes which hybridize to the same target sequence in adjacent locations on said target sequence, said probes hybridizing specifically to SEQ ID NO 1 or SEQ ID NO 2 or homologues, or to their RNA form wherein T is replaced by U, or to their complementary form, wherein there are no more than 25 nucleotides between said probes along said target sequence.

6. (Original) A set of two or three polynucleotide probes according to claim 5 consisting of any combinations of Table 3.

7. (Currently Amended) A composition comprising at least one nucleic acid molecule according to claim 1 and/or a set of two polynucleotide probes, said probes comprising more than 10 contiguous nucleotides.

8. (Previously Presented) A method of detecting and/or identification of *Enterococcus* species in a sample comprising hybridizing a nucleic acid molecule of claim 3 to nucleic acid sequences of said sample and detecting said hybridization.

9. (Previously Presented) The method of claim 8 wherein said *Enterococcus* species is at least one of *E. faecalis* and *E. faecium*.

10. (Previously Presented) A method according to claim 8 for detection and/or identification of *Enterococcus* species in a sample comprising the steps of:

(i) if need be releasing, isolating and/or concentrating the polynucleic acids in the sample;

(ii) if need be amplifying the 16S-23S rRNA spacer region, or a fragment comprising a *Enterococcus* species-specific polynucleic acid, with at least one suitable primer pair;

(iii) hybridizing the polynucleic acids of step (i) or (ii) with at least one polynucleotide probe of claim 3,

(iv) detecting the hybrids formed, and

(v) interpreting the signal(s) obtained and inferring the presence of *Enterococcus* species and/or identifying the *Enterococcus* species in the sample.

11. (Original) A method according to claim 10 wherein a suitable primer pair consists any combination of a forward primer polynucleotide selected from the group consisting of SEQ ID NO 3, 4, 5, 6, 7, 8, 9, 10 or 11 and their homologues, and a reverse primer polynucleotide selected from the group consisting of SEQ ID NO 12, 13, 14, 15, 16, 17, 18, 19, 20 or 21 and their homologues.

12. (Previously Presented) A method according to claim 10 wherein said at least one probe comprises two polynucleotide probes.

13. (Previously Presented) A method according to claim 12 wherein said at least one probe comprises a set of two polynucleotide probes which hybridize to the same target sequence in adjacent locations on said target sequence, wherein there are no more than 25 nucleotides between said probes along the hybridized polynucleic acid sequence.

14. (Previously Presented) A method according to claim 12 wherein the two polynucleotide probes consist of any combination of polynucleotides of Table 3.

15. (Previously Presented) A kit for detection and/or identification of *Enterococcus* species comprising the following components:

at least one nucleic acid molecule according to claim 3, and

a hybridization buffer, or components necessary for producing said buffer.